AU 1806

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,283

DATE: 05/17/96
TIME: 15:48:02

INPUT SET: S10587.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

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1                              SEQUENCE LISTING
2
3    (1)    General Information:
4                                              Does Not Comply
5    (i)APPLICANT: Evans, Mark J.              Corrected Diskette Needed
6                 Matis, Louis A.
7                 Mueller, Eileen Elliott
8                 Nye, Steven H.
9                 Rollins, Scott
10                Rother, Russell P.
11                Springhorn, Jeremy P.
12                Squinto, Stephen P.
13                Thomas, Thomas C.
14                Wilkins, James A.
15
16   (ii)TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
17       OF INFLAMMATORY DISEASES
18
19       (iii) NUMBER OF SEQUENCES: 26
20
21   (iv) CORRESPONDENCE ADDRESS:
22   (A)ADDRESSEE:  Seth A. Fidel
23   (B)STREET:   25 Science Park (Alexion)
24   (C)CITY:  New Haven
25   (D)STATE:  Connecticut
26   (E)COUNTRY:  USA
27   (F)ZIP:  06511
28
29   (v)COMPUTER READABLE FORM:
30   (A)MEDIUM TYPE:  3.5 inch, 1.4Mb storage
31   (B)COMPUTER:  Macintosh Cetris 610
32   (C)OPERATING SYSTEM:  System 7
33   (D)SOFTWARE:  WordPerfect 3.0
34   (vi)CURRENT APPLICATION DATA:
35   (A)APPLICATION NUMBER:08/487,283
36   (B)FILING DATE: June 7, 1995
37      (vii)PRIOR APPLICATION DATA:
38   (A)APPLICATION NUMBER: US 08/236,208
39   (B)FILING DATE:  02-MAY-1994
40
41      (viii)ATTORNEY/AGENT INFORMATION:
42   (A)NAME:  Seth A. Fidel.
43   (B)REGISTRATION NUMBER: 38,449
44   (C)REFERENCE/DOCKET NUMBER:  ALX-152.1 CIP
45   (ix)TELECOMMUNICATION INFORMATION:
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,283*

DATE: 05/17/96
TIME: 15:48:06

INPUT SET: S10587.raw

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46   (A)TELEPHONE:  (203)776-1790
47   (B)TELEFAX:   (203)772-3655
48
49
50
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place this heading here.

ERRORED SEQUENCES FOLLOW:

(ii) Molecule type:

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51   (2)  INFORMATION FOR SEQ ID NO:1:
52   (i)  SEQUENCE CHARACTERISTICS:
53   (A)  LENGTH:  21 amino acids
54   (B)  TYPE:  Amino Acid
55   (C)  STRANDEDNESS:  Single
56   (D)  TOPOLOGY:  Linear
-->  57   (A)  DESCRIPTION:  KSSKC peptide
58   (iii) HYPOTHETICAL:  No
59   (iv) ANTI-SENSE:  No
60
61   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:1:
62
63   Val Ile Asp His Gln Gly Thr Lys Ser Ser
64                       5                   10
65
66   Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
67                       15                  20
68
69
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70   (2)  INFORMATION FOR SEQ ID NO:2:
71        (i)  SEQUENCE CHARACTERISTICS:
-->  72        (A)  LENGTH:  1658 Amino Acids
73        (B)  TYPE:  Amino Acid
74        (C)  STRANDEDNESS:  Single
75        (D)  TOPOLOGY:  Linear
-->  76   (A)DESCRIPTION:  Pro-C5 Polytpeptide
77   (iii) HYPOTHETICAL:  No
78   (iv) ANTI-SENSE:  No
79   (vi) ORIGINAL SOURCE:
80        (A)  ORGANISM:  Homo sapiens
81   (x)  PUBLICATION INFORMATION:
82        (A)  AUTHORS:   Haviland, D.L.
83                        Haviland, J.C.
84                        Fleischer, D.T.
85                        Hunt, A.
86                        Wetsel, R.A.
87
88        (B)  TITLE:  Complete cDNA Sequence of Human
89                     Complement Pro-C5
90        (C)  JOURNAL: Journal of Immunology
91        (D)  VOLUME:  146
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include in this count the negative numbers (1676)

throughout

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92              (F) PAGES:  362-368
93              (G) DATE:  1991
94
95
96    (xi) SEQUENCE DESCRIPTION:   SEQ ID NO:2:
97
98                    Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
99                            -15             -10
100
101   Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
102            -5              -1              5
103
104   Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
105            10              15              20
106
107   Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
108                25              30
109
110   Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
111    35              40              45
112
113   Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
114        50              55              60
115
116   Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
117            65              70              75
118
119   Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
120            80              85              90
121
122   Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
123            95              100
124
125   Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
126   105              110             115
127
128   Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
129        120             125             130
130
131   Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
132        135             140             145
133
134   Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
135            150             155             160
136
137   His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
138            165             170
139
140   Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
141   175             180             185
142
143   Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys
144        190             195             200
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145
146    Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu
147            205             210                 215
148
149    Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
150            220             225                 230
151
152    Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
153            235             240
154
155    Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
156    245             250             255
157
158    Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
159        260             265                 270
160
161    Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
162            275             280                 285
163
164    Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
165            290             295                 300
166
167    Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
168            305             310
169
170    Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
171    315             320             325
172
173    Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
174        330             335                 340
175
176    Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
177            345             350                 355
178
179    Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
180            360             365                 370
181
182    Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
183            375             380
184
185    Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
186    385             390             395
187
188    Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
189        400             405                 410
190
191    Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
192            415             420                 425
193
194    Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
195            430             435                 440
196
197    Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn
```

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198                    445                    450
199
200   His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
201   455                 460                 465
202
203   Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn
204       470                 475                 480
205
206   Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
207           485                 490                 495
208
209   Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
210           500                 505                 510
211
212   Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
213               515                 520
214
215   Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
216   525                 530                 535
217
218   Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
219       540                 545                 550
220
221   Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro
222       555                 560                 565
223
224   Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
225               570                 575                 580
226
227   Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
228               585                 590
229
230   Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
231   595                 600                 605
232
233   Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Gly Leu
234       610                 615                 620
235
236   Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
237       625                 630                 635
238
239   Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
240           640                 645                 650
241
242   Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
243               655                 660
244
245   Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
246   665                 670                 675
247
248   Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
249       680                 685                 690
250
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251   Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
252           695                 700                 705
253
254   Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
255           710                 715                 720
256
257   Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu
258               725             730
259
260   His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg
261   735             740                 745
262
263   Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val
264       750             755                 760
265
266   Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu
267       765             770                 775
268
269   Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly
270           780             785                 790
271
272   Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp
273           795             800
274
275   Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly
276   805             810             815
277
278   Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr
279       820             825             830
280
281   Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly
282       835             840             845
283
284   Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr
285           850             855                 860
286
287
288   Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
289           865             870
290
291   Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
292   875             880                 885
293
294   Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
295       890             895                 900
296
297   Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
298       905             910                 915
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300   Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
301       920             925                 930
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303   Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg
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INPUT SET: S10587.raw

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306   Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
307   945                 950                 955
308
309   Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
310       960                 965                 970
311
312   Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
313           975                 980                 985
314
315   Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
316           990                 995                 1000
317
318   Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
319               1005                1010
320
321   Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
322   1015                1020                1025
323
324   Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
325       1030                1035                1040
326
327   Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
328           1045                1050                1055
329
330   Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
331               1060                1065                1070
332
333   Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
334               1075                1080
335
336   Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
337   1085                1090                1095
338
339   Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
340       1100                1105                1110
341
342   Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
343           1115                1120                1125
344
345   Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
346               1130                1135                1140
347
348   Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
349               1145                1150
350
351   Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
352   1155                1160                1165
353
354   Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
355       1170                1175                1180
356
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357   Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
358           1185              1190              1195
359
360   Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
361           1200              1205              1210
362
363   Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
364           1215              1220
365
366   Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
367   1225              1230              1235
368
369   Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
370       1240              1245              1250
371
372   Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
373           1255              1260              1265
374
375   Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
376           1270              1275              1280
377
378   Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
379               1285              1290
380
381   Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
382   1295              1300              1305
383
384   Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
385       1310              1315              1320
386
387   Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
388           1325              1330              1335
389
390   Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
391               1340              1345              1350
392
393   Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
394               1355              1360
395
396   Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
397   1365              1370              1375
398
399   Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
400       1380              1385              1390
401
402   Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
403           1395              1400              1405
404
405   Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
406           1410              1415              1420
407
408   Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
409               1425              1430
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410
411   Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
412   1435              1440              1445
413
414   Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
415      1450              1455              1460
416
417   Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
418          1465              1470              1475
419
420   Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
421              1480              1485              1490
422
423   Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
424              1495              1500
425
426   Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
427   1505              1510              1515
428
429   Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
430      1520              1525              1530
431
432   Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
433          1535              1540              1545
434
435   Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
436              1550              1555              1560
437
438   Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
439              1565              1570
440
441   Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
442   1575              1580              1585
443
444   Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
445      1590              1595              1600
446
447   Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
448          1605              1610              1615
449
450   Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
451              1620              1625              1630
452
453   Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
454              1635              1640
455
456   Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
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458
459
460
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2493   (2) INFORMATION FOR SEQ ID NO:19:
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INPUT SET: S10587.raw

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 2494          (i) SEQUENCE CHARACTERISTICS:
 2495              (A) LENGTH:  813 base pairs        only 783 are shown.
 2496              (B) TYPE:  Nucleic Acid
 2497              (C) STRANDEDNESS:  Double
 2498              (D) TOPOLOGY:  linear
 2499          (ii) MOLECULE TYPE:  Other nucleic acid
 2500              (A) DESCRIPTION: N19/8 scFv (His Tagged)
 2501
 2502
 2503    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:19:
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 2505    ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30
 2506    Met Ala Asn Ile Val Leu Thr Gln Ser Pro
 2507     1               5                   10
 2508
 2509    GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60
 2510    Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
 2511                    15                  20
 2512
 2513    GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT (120) 90?
 2514    Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
 2515                    25                  30
 2516
 2517    GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150 ?
 2518    Val Asp Ser Tyr Asp Asn Ser Phe Met His
 2519                    35                  40
 2520
 2521    TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180 ?
 2522    Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 2523                    45                  50
 2524
 2525    AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210
 2526    Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu
 2527                    55                  60
 2528
 2529    GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240
 2530    Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 2531                    65                  70
 2532
 2533    AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270
 2534    Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr
 2535                    75                  80
 2536
 2537    ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300
 2538    Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
 2539                    85                  90
 2540
 2541    ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330
 2542    Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val
 2543                    95                  100
 2544
 2545    CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360
 2546    Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu
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2547                          105                       110
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2549   GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390
2550   Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser
2551                          115                       120
2552
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2554   Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
2555                          125                       130
2556
2557   GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
2558   Asp Val Lys Leu Val Glu Ser Gly Gly Asp
2559                          135                       140
2560
2561   TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
2562   Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
2563                          145                       150
2564
2565   TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
2566   Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
2567                          155                       160
2568
2569   AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
2570   Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
2571                          165                       170
2572
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2575                          175                       180
2576
2577   ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
2578   Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
2579                          185                       190
2580
2581   CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
2582   Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
2583   ·         .           195                       200
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2585   TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
2586   Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
2587                          205                       210
2588
2589   CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690
2590   Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
2591                          215                       220
2592
2593   ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720
2594   Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr
2595                          225                       230
2596
2597   TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750
2598   Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp
2599                          235                       240
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2601   GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780
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2603                   245                 250
2604
2605   TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810
2606   Ser Ser Leu Glu His His His His His His
2607                   255                 260
2608
2609   TGA                                     813
2610
2611
2612
```

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/236,208

TEAM 2

DATE: 01/05/96
TIME: 15:16:30

INPUT SET: S8120.raw

Gambel 16   IPC

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

not a sequence case

```
 1                               SEQUENCE LISTING
 2
 3    (1)     General Information:                See marked-up
 4                                                  notes
 5    (i)APPLICANT: Evans, Mark J.
 6                  Matis, Louis A.
 7                  Mueller, Eileen Elliott
 8                  Nye, Steven H.
 9                  Rollins, Scott
10                  Rother, Russell P.
11                  Springhorn, Jeremy P.
12                  Squinto, Stephen P.
13                  Thomas, Thomas C.
14                  Wilkins, James A.
15
16    (ii)TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
17         OF INFLAMMATORY DISEASES
18
19        (iii) NUMBER OF SEQUENC
20
21    (iv) CORRESPONDENCE ADDRES
22    (A)ADDRESSEE:  Seth A. Fid
23    (B)STREET:   25 Science Pa         LOC
24    (C)CITY:  New Haven
25    (D)STATE:  Connecticut
26    (E)COUNTRY:  USA
27    (F)ZIP:  06511                    18C2
28
29    (v)COMPUTER READABLE FOF
30    (A)MEDIUM TYPE:  3.5 inc
31    (B)COMPUTER:  Macintosh
32    (C)OPERATING SYSTEM:  S
33    (D)SOFTWARE:  WordPerfe
34    (vi)CURRENT APPLICATIO1
35    (A)APPLICATION NUMBER:
36    (B)FILING DATE: June 7
37       (vii)PRIOR APPLICA7
38    (A)APPLICATION NUMBER
39    (B)FILING DATE:  02-MAY-1994
40
41       (viii)ATTORNEY/AGENT INFORMATION:
42    (A)NAME:  Seth A. Fidel.
43    (B)REGISTRATION NUMBER: 38,449
44    (C)REFERENCE/DOCKET NUMBER:  ALX-152.1 CIP
45    (ix)TELECOMMUNICATION INFORMATION:
```

--> (line 35)

's k was fitted for application